Amendments to the Specification

Page 1, immediately after the title, please insert:

This application is a U.S. national stage of International Application No. PCT/JP2004/017306 filed November 19, 2004.

Page 2, paragraph [0007], at line 31 to page 3, line 8, please rewrite as follows:

[0007] The ~~c-fos~~ c-jun gene was isolated as a human homolog of which amino acid sequence indicates more than 80% identity or more with an oncogene, v-jun which is possessed by avian sarcoma virus 17 (the v-jun afterward became known to be derived form chicken genome and be conserved among the many species) (Non-patent document 15). The c-jun is a transcription control facter detected in many cytomas as a typical immediate early gene in connection with a proliferataion stimulus. As known falimy genes, junB and junC are known. Generation of a null-mutated mouse by gene targeting and analysis conducted by Hilberg et al. confirmed that c-Jun-lacking mice exhibit impaired hepatogenesis and embryonically lethal. This suggested that an essential involvement of the c-jun gene in hepatogenesis (Non-patent document 16).

Page 6, paragraph [0014], at lines 16-18, please rewrite as follows:

[0014] (2) The inhibitor according to ~~(2)~~ (1), wherein the protein as the active ingredient comprises any one of the amino acid sequences of SEQ ID NOS: 1 to 69.

Page 33, paragraph [0131], at line 29 to page 34, line 11, please rewrite as follows:

[0131] Among the proteins of the present invention, the proteins having any one of the amino acid sequences of SEQ ID NOS: 1 to ~~124~~ 125 are proteins for which it has been found that they interact with the c-Jun protein, i.e., form a complex, as described in the examples mentioned below. For proteins, existence of a mutant having the same function is generally expected. Further, by suitably modifying an amino acid sequence of a protein, a mutant having the same function can be obtained. Therefore, proteins that have any one of the amino acid sequences of SEQ ID NOS: 1 to ~~124~~ 125 including

deletion, substitution or addition of one or several amino acid residues and interact with the c-Jun protein also fall within the scope of the proteins of the present invention. The term "several" used herein means preferably within 5, more preferably within 2. Further, proteins that show a homology of usually 15% or more, preferably 90% or more, more preferably 95% or more to any one of the amino acid sequences of SEQ ID NOS: 1 to ~~124~~ 125 and interact with the c-Jun protein also fall within the scope of the protein of the present invention.

Page 34, paragraph [0134], at line 26 to page 35, line 14, please rewrite as follows:

[0134] The nucleic acids of the present invention are nucleic acids encoding the proteins of the present invention. The nucleic acids are usually RNA or DNA. Examples of the nucleic acids of the present invention include nucleic acids having any one of the nucleotide sequences of SEQ ID NOS: 126 to ~~254~~ 255. These nucleic acids are nucleic acids of which nucleotide sequences were determined in the examples mentioned below. For a gene, existence of a gene encoding the same product, but having a different nucleotide sequence, or a gene encoding a mutant having the same function is expected. Further, by suitably modifying a nucleotide sequence, a gene encoding the same product or a mutant having the same function can be obtained. Therefore, nucleic acids having a nucleotide sequence similar to any one of the nucleotide sequences of SEQ ID NOS: 126 to ~~254~~ 255 and encoding a protein that interacts with the c-Jun protein also fall within the scope of the nucleic acids of the present invention. Examples of such nucleic acids having a similar nucleotide sequence include nucleic acids that hybridize with a nucleic acid having a nucleotide sequence complementary to any one of the nucleotide sequences of SEQ ID NOS: 126 to ~~254~~ 255 under a stringent condition, and nucleic acids having a nucleotide sequence showing a homology of usually 16% or more, preferably 90% or more, more preferably 95% or more to any one of the nucleotide sequences of SEQ ID NOS: 126 to ~~254~~ 255.

Page 58, paragraph [0202], at lines 14-33, please rewrite as follows:

[0202] The screening method of the present invention further comprises the preparation step of preparing a prey selected in the selection step, and it is preferable to repeat the detection step, selection step and preparation step by using the prepared prey instead of or together with the bait used in the detection step. In this embodiment, the method is constituted by, for example, 1) the step of cell-free cotranslation in a cell-free translation system in which a prey and a bait cause an interaction, 2) the step of screening for detecting a prey interacting with the bait, 3) the step of examining and analyzing the prey, and 4) the step of repeating the steps from 1) by using the prey examined and analyzed in 3), as shown in Fig. ~~10~~ 11. The steps of 1) and 2) correspond to the detection step and selection step, and the step of 3) corresponds to the preparation step. That is, the step of contacting a prey to the bait in the detection step corresponds to the step of the cell-free cotranslation, and the steps of detecting and selecting a complex in the detection step correspond to the step of screening.

Page 87, paragraph [0300], at lines 8-12, please rewrite as follows:

[0300] As a result, it could be confirmed that the proteins of SEQ ID NOS: ~~2~~ 18 (SNAP19), ~~71~~ 76 (KINN), ~~89~~ 93 [[(]] (Kif5a), ~~96~~ 99 (Eef1d), ~~101~~ 102 [[(]] (Nef3), 106 (Jip-c3.1), 110 (Jip-c1), 113 (EB2), 115 (Cspg6), 117 (Mapk8ip3), 119 (Jip-c3.2) and 123 (Jip-c8) directly interacted with c-Jun.